1: BE949139. Reports UI-M-BH3-avh-f-01...[gi:10526898] Link

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LOCUS       BE949139                606 bp    mRNA    linear   EST 03-OCT-2000
DEFINITION  UI-M-BH3-avh-f-01-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-avh-f-01-0-UI 3', mRNA sequence.
ACCESSION   BE949139
VERSION     BE949139.1  GI:10526898
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 606)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..606
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH3-avh-f-01-0-UI"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_M_S4"
                     /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI;
                     The NIH_BMAP_M_S4 library is a subtracted library of a
                     series, ultimately  derived from a mixture of individually
                     tagged normalized libraries from  ten regions of the mouse
                     brain (cerebellum, brain stems, olfactory  bulbs,
                     hypothalamus, cortex, amygdala, basal ganglia, pineal
                     gland,  striatum, hipoccampus) after a series of
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subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

ORIGIN

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      121 ctgaagggag gagcctttct cttggagagg atcctcgatg agcctggccg aggcccgggg
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Nov 21 2005 12:16:20